



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/135,238

Art Unit / Team No.

1643

Date Processed by STIC:

6/18/09

RECEIVED
APR 18 2000
TG 1600 MAIL ROOM

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/135,238

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length
Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 Skipped Sequences (OLD RULES)
Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(x1) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES)
Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>-Organism (NEW RULES)
Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>-Feature (NEW RULES)
Sequence(s) are missing the <220>-Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>-ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing numerical identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

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N/A

1643

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/135,238

DATE: 06/18/1999
TIME: 15:43:31

Input Set: I135238.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Nolan, Garry P
2 Hitoshi, Yasumichi
3 <120> TITLE OF INVENTION: TOSO
4 <130> FILE REFERENCE: A-65635-1/DJB/RMS
5 <140> CURRENT APPLICATION NUMBER: US/09/135,238
6 <141> CURRENT FILING DATE: 1998-08-17
7 <150> EARLIER APPLICATION NUMBER: 60/066,063
8 <151> EARLIER FILING DATE: 1997-11-17
9 <160> NUMBER OF SEQ ID NOS: 31
10 <170> SOFTWARE: PatentIn Ver. 2.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 1910
13 <212> TYPE: DNA
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18 cctgaggatc ctcccagaag taaaggtaga gggggagctg gcgcgatcag ttaccatcaa 180
19 atgcccactt cctgaaatgc atgtgaggat atatctgtgc cgggagatgg ctggatctgg 240
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22 aagtgcacgc ggagtcctat cctgcggagc gggcatgaac acagaccggg gaaagaccca 420
23 gaaagtccac ctgaatgtcc acagtgaata cgagccatca tgggaagagc agccaatgcc 480
24 tgagactcca aaatgggttc atctgcctta ttgttccag atgcctgcac atgccagttc 540
25 ttccaaatcc gtaaccagag ttaccacacc agctcaagg ggcaagggtc ctccagtgca 600
26 ccactcctcc ccaccacccc aaatcaccca ccgcctcga gtgtccagag catcttcagt 660
27 agcaggtgac aagccccgaa ctttcctgcc atccactaca gcttcaaaaa tctcagctct 720
28 ggaggggctg ctcaagcccc agacgccacg ctacaaccac cacaccaggc tgcacaggca 780
29 gagagcactg gactatggct cacagtctgg gagggaaagg caaggatttc acatctgat 840
30 ccgacacatc ctggcccttt tctgtctggc acttctgggg ctggtggtga aaaggcgctg 900
31 tgaaaggagg aaagccctct ccaggcgggc ccgcgcagt ggcgtgagga tgcgcgccct 960
32 ggagagctcc cagaggcccc gcgggtcgcc gcgaccgcgc tcccaaaaca acatctacag 1020
33 cgactccccc cggcgcgctc tggagcggac gctgcaggca caggggcgat ccccgctccc 1080
34 ggccccggag cgccgtgtgc cccgcgcccg ctgcagggtg ctgaatctcc ctggctccat 1140
35 gcccaatcc agttgacagg ctgtgaatac accaccagcc tggcccgcat 1200
36 atggaggaca gtgattcaga tgactacatc aatgttctct cctgacaact ccccgctat 1260
37 cccccacccc caggctcgga ctgtgtgtgc aaggagtctc atctatctgc tgatgtccaa 1320
38 taactgtctc atgtgttctc agagccctca tcacttccca tgccccatct cgactcccat 1380
39 ccccatctat ctgtggccct gagcatggct ctgccccagc gtgcttctgc acactctggc 1440
40 agccccctgt agttgacagg taagctgtag gcattgtagc caattgtccc aatgccaact 1500
41 gcttctcttc caagccctgc aacagactgt gggatttgca gagtgtttct tccatgtct 1560
42 tgaccacagc gtgtgtgtgc tgccaggctc tagatcacat ggcatcaggc tggggcagag 1620
43 gcatagctat gtctctgggc atccttccca gggttgggtc ttacacaaat agaaggtctc 1680
44 tgctctgagt tatgtgagct gcctcagccc catggactaa cagggggtct ggtataaaca 1740

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45      ctctctggaaa cgcctttgccc ctgattccaaa tgttagcact tgctagttaa cgtctactta 1800
46      tctcaagttc tatgtctaaag gcaatttatc ttgatgtgat gataaaccaa accttattagc 1860
47      aagatatgca tatatatcca taaattctct ttactctgtc tccatccttt      1910
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54      1          5          10          15
55      Leu Arg Ile Leu Pro Glu Val Lys Val Glu Gly Glu Leu Gly Gly Ser
56      20          25          30
57      Val Thr Ile Lys Cys Pro Leu Pro Glu Met His Val Arg Ile Tyr Leu
58      35          40          45
59      Cys Arg Glu Met Ala Gly Ser Gly Thr Cys Gly Thr Val Val Ser Thr
60      50          55          60
61      Thr Asn Phe Ile Lys Ala Glu Tyr Lys Gly Arg Val Thr Leu Lys Gln
62      65          70          75          80
63      Tyr Pro Arg Lys Asn Leu Phe Leu Val Glu Val Thr Gln Leu Thr Glu
64      85          90          95
65      Ser Asp Ser Gly Val Tyr Ala Cys Gly Ala Gly Met Asn Thr Asp Arg
66      100         105         110
67      Gly Lys Thr Gln Lys Val Thr Leu Asn Val His Ser Glu Tyr Glu Pro
68      115         120         125
69      Ser Trp Glu Glu Gln Pro Met Pro Glu Thr Pro Lys Trp Phe His Leu
70      130         135         140
71      Pro Tyr Leu Phe Gln Met Pro Ala Tyr Ala Ser Ser Ser Lys Phe Val
72      145         150         155         160
73      Thr Arg Val Thr Thr Pro Ala Gln Arg Gly Lys Val Pro Pro Val His
74      165         170         175
75      His Ser Ser Pro Thr Thr Gln Ile Thr His Arg Pro Arg Val Ser Arg
76      180         185         190
77      Ala Ser Ser Val Ala Gly Asp Lys Pro Arg Thr Phe Leu Pro Ser Thr
78      195         200         205
79      Thr Ala Ser Lys Ile Ser Ala Leu Glu Gly Leu Leu Lys Pro Gln Thr
80      210         215         220
81      Pro Ser Tyr Asn His His Thr Arg Leu His Arg Gln Arg Ala Leu Asp
82      225         230         235         240
83      Tyr Gly Ser Gln Ser Gly Arg Glu Gly Gln Gly Phe His Ile Leu Ile
84      245         250         255
85      Pro Thr Ile Leu Gly Leu Phe Leu Leu Ala Leu Leu Gly Leu Val Val
86      260         265         270
87      Lys Arg Ala Val Glu Arg Arg Lys Ala Leu Ser Arg Arg Ala Arg Arg
88      275         280         285
89      Leu Ala Val Arg Met Arg Ala Leu Glu Ser Ser Gln Arg Pro Arg Gly
90      290         295         300
91      Ser Pro Arg Pro Arg Ser Gln Asn Asn Ile Tyr Ser Ala Cys Pro Arg
92      305         310         315         320
93      Arg Ala Arg Gly Ala Asp Ala Ala Gly Thr Gly Glu Ala Pro Val Pro
94      325         330         335

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95      Gly Pro Gly Ala Pro Leu Pro Pro Ala Pro Leu Gln Val Ser Glu Ser
96              340              345              350
97      Pro Trp Leu His Ala Pro Ser Leu Lys Thr Ser Cys Glu Tyr Val Ser
98              355              360              365
99      Leu Tyr His Gln Pro Ala Ala Met Met Glu Asp Ser Asp Ser Asp Asp
100             370              375              380
101      Tyr Ile Asn Val Pro Ala
102             385              390
103      <210> SEQ ID NO 3
104      <211> LENGTH: 73
105      <212> TYPE: PRT
106      <213> ORGANISM: Homo sapiens
107      <400> SEQUENCE: 3
108      Val Thr Ile Lys Cys Pro Leu Pro Glu Met His Val Arg Ile Tyr Leu
109              1              5              10              15
110      Cys Arg Glu Met Ala Gly Ser Gly Thr Cys Gly Thr Val Val Ser Thr
111              20              25              30
112      Thr Asn Phe Ile Lys Ala Glu Trp Lys Gly Arg Val Thr Leu Lys Gln
113              35              40              45
114      Tyr Pro Arg Lys Asn Leu Phe Leu Val Glu Val Thr Gln Leu Thr Glu
115              50              55              60
116      Ser Asp Ser Gly Val Tyr Ala Cys Gly
117              65              70
118      <210> SEQ ID NO 4
119      <211> LENGTH: 79
120      <212> TYPE: PRT
121      <213> ORGANISM: Homo sapiens
122      <400> SEQUENCE: 4
123      Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Thr Phe Ser Asn Asp Tyr
124              1              5              10              15
125      Tyr Thr Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly
126              20              25              30
127      Tyr Val Phe Tyr His Gly Thr Ser Asp Asp Thr Thr Pro Leu Arg Ser
128              35              40              45
129      Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg
130              50              55              60
131      Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
132              65              70              75
133      <210> SEQ ID NO 5
134      <211> LENGTH: 73
135      <212> TYPE: PRT
136      <213> ORGANISM: Homo sapiens
137      <400> SEQUENCE: 5
138      Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn
139              1              5              10              15
140      Tyr Ala Asn Trp Val Gln Gln Lys Pro Asp His Leu Phe Thr Gly Ile
141              20              25              30
142      Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly
143              35              40              45
144      Ser Leu Ile Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Thr

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146      Glu Asp Glu Ala Ile Tyr Phe Cys Ala
147          65          70
148 <210> SEQ ID NO 6
149 <211> LENGTH: 72
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
152 <400> SEQUENCE: 6
153      Thr Ser Leu Asn Cys Thr Phe Ser Asp Ser Ala Ser Gln Tyr Phe Trp
154          1          5          10          15
155      Trp Tyr Arg Gln His Ser Gly Lys Ala Pro Lys Ala Leu Met Ser Ile
156          20          25          30
157      Phe Ser Asn Gly Glu Lys Glu Glu Gly Arg Phe Thr Ile His Leu Asn
158          35          40          45
159      Lys Ala Ser Leu His Phe Ser Leu His Ile Arg Asp Ser Gln Pro Ser
160          50          55          60
161      Asp Ser Ala Leu Tyr Leu Cys Ala
162          65          70
163 <210> SEQ ID NO 7
164 <211> LENGTH: 75
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 7
168      Val Thr Leu Arg Cys Lys Pro Ile Ser Gly His Asn Ser Leu Phe Trp
169          1          5          10          15
170      Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu Ile Tyr Phe Asn
171          20          25          30
172      Asn Asn Val Pro Ile Asp Asp Ser Gly Met Pro Glu Asp Arg Phe Ser
173          35          40          45
174      Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser
175          50          55          60
176      Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala
177          65          70          75
178 <210> SEQ ID NO 8
179 <211> LENGTH: 74
180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
182 <400> SEQUENCE: 8
183      Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His
184          1          5          10          15
185      Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe
186          20          25          30
187      Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg
188          35          40          45
189      Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys
190          50          55          60
191      Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu
192          65          70
193 <210> SEQ ID NO 9
194 <211> LENGTH: 80

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/135,238

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195 <212> TYPE: PRT
196 <213> ORGANISM: Homo sapiens
197 <400> SEQUENCE: 9
198 Ala Lys Met Ser Cys Glu Ala Lys Thr Phe Pro Lys Gly Thr Thr Ile
199 1 5 10 15
200 Tyr Trp Leu Arg Glu Leu Gln Asp Ser Asn Lys Asn Lys His Phe Glu
201 20 25 30
202 Phe Leu Ala Ser Arg Thr Ser Thr Lys Gly Ile Lys Tyr Gly Glu Arg
203 35 40 45
204 Val Lys Lys Asn Met Thr Leu Ser Phe Asn Ser Thr Leu Pro Phe Leu
205 50 55 60
206 Lys Ile Met Asp Val Lys Pro Glu Asp Ser Gly Phe Tyr Phe Cys Ala
207 65 70 75 80

208 <210> SEQ ID NO 10
209 <211> LENGTH: 76
210 <212> TYPE: PRT
211 <213> ORGANISM: Homo sapiens
212 <400> SEQUENCE: 10
213 Val Thr Ile Thr Cys Pro Phe Thr Tyr Ala Thr Arg Gln Leu Lys Lys
214 1 5 10 15
215 Ser Phe Tyr Lys Val Glu Asp Gly Glu Leu Val Leu Ile Ile Asp Ser
216 20 25 30
217 Ser Ser Lys Glu Ala Lys Asp Pro Arg Tyr Lys Gly Arg Ile Thr Leu
218 35 40 45
219 Gln Ile Gln Ser Thr Thr Ala Lys Glu Phe Thr Val Thr Leu Lys His
220 50 55 60
221 Leu Gln Leu Asn Asp Ala Gly Gln Tyr Val Cys Gln
222 65 70 75

223 <210> SEQ ID NO 11
224 <211> LENGTH: 84
225 <212> TYPE: PRT
226 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <221> NAME/KEY: UNSURE
229 <222> LOCATION: (53)
230 <223> OTHER INFORMATION: F can be either V or I or F
231 <220> FEATURE:
232 <221> NAME/KEY: UNSURE
233 <222> LOCATION: (79)
234 <223> OTHER INFORMATION: A can be either G or A
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
237 <400> SEQUENCE: 11

W--> 238 Val Thr Leu Thr Cys Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
239 1 5 10 15
W--> 240 Xaa Xaa Phe Xaa Trp Xaa Arg Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
241 20 25 30 35 40
W--> 242 Leu Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
243 35 40 45
W--> 244 Tyr Xaa Xaa Arg Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

"Phe" can only represent itself, nothing else. Use "Xaa" and explain it.
L2207-L2237 section

SAME ERROR

see item 10 on Ena Summary Sheet

Input Set: I135238.RAW

Line ? Error/Warning

Original Text

238 W "N" or "Xaa" used: Feature required
240 W "N" or "Xaa" used: Feature required
242 W "N" or "Xaa" used: Feature required
244 W "N" or "Xaa" used: Feature required
246 W "N" or "Xaa" used: Feature required
248 W "N" or "Xaa" used: Feature required

Val Thr Leu Thr Cys Xaa Xaa Ser Xaa Xaa X
Xaa Xaa Phe Xaa Trp Xaa Arg Gln Xaa Xaa X
Leu Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa X
Tyr Xaa Xaa Arg Phe Xaa Xaa Xaa Xaa X
Xaa Phe Ser Leu Thr Ile Xaa Asn Xaa Xaa X
Tyr Xaa Cys Ala